

#9



1600

RAW SEQUENCE LISTING

DATE: 11/20/2002

PATENT APPLICATION: US/09/658,677

TIME: 17:58:57

Input Set : N:\Cr3\RULE60\09658677.raw

Output Set: N:\CRF4\11202002\I658677.raw

ENTERED

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Sheppard, Paul O.
 7 (ii) TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
 8 AND MATERIALS AND METHODS FOR MAKING THEM
 10 (iii) NUMBER OF SEQUENCES: 18
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: ZymoGenetics, Inc.
 14 (B) STREET: 1201 Eastlake Avenue East
 15 (C) CITY: Seattle
 16 (D) STATE: WA
 17 (E) COUNTRY: USA
 18 (F) ZIP: 98102
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Diskette
 22 (B) COMPUTER: IBM Compatible
 23 (C) OPERATING SYSTEM: DOS
 24 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 26 (vi) CURRENT APPLICATION DATA:
 C--> 27 (A) APPLICATION NUMBER: US/09/658,677
 C--> 28 (B) FILING DATE: 08-Sep-2000
 29 (C) CLASSIFICATION:
 31 (vii) PRIOR APPLICATION DATA:
 32 (A) APPLICATION NUMBER: US/09/072,384
 33 (B) FILING DATE:
 35 (viii) ATTORNEY/AGENT INFORMATION:
 36 (A) NAME: Parker, Gary E
 37 (B) REGISTRATION NUMBER: 31,648
 38 (C) REFERENCE/DOCKET NUMBER: 97-16C1
 40 (ix) TELECOMMUNICATION INFORMATION:
 41 (A) TELEPHONE: 206-442-6673
 42 (B) TELEFAX: 206-442-6678
 43 (C) TELEX:
 46 (2) INFORMATION FOR SEQ ID NO: 1:
 48 (i) SEQUENCE CHARACTERISTICS:
 49 (A) LENGTH: 1634 base pairs
 50 (B) TYPE: nucleic acid
 51 (C) STRANDEDNESS: double
 52 (D) TOPOLOGY: linear
 54 (ix) FEATURE:
 60 (A) NAME/KEY: Signal Sequence
 57 (B) LOCATION: 105...1280
 58 (D) OTHER INFORMATION:

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64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66  GGCACGAGGG GGAGCCGCGC GCTCTCTCCC GGCGCCACAC CCTGTCTGAG CGGCGCAGCG      60
67  AGCCGCGGCC CGGGCGGGCT GCTCGGCGCG GAACAGTGCT CGGC ATG GCA GGG ATT      116
68                                     Met Ala Gly Ile
71  CCA GGG CTC CTC TTC CTT CTC TTC TTT CTG CTC TGT GCT GTT GGG CAA      164
72  Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys Ala Val Gly Gln
73  -15 -10 -5 1
75  GTG AGC CCT TAC AGT GCC CCC TGG AAA CCC ACT TGG CCT GCA TAC CGC      212
76  Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp Pro Ala Tyr Arg
77                                     5 10 15
79  CTC CCT GTC GTC TTG CCC CAG TCT ACC CTC AAT TTA GCC AAG CCA GAC      260
80  Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala Lys Pro Asp
81 20 25 30
83  TTT GGA GCC GAA GCC AAA TTA GAA GTA TCT TCT TCA TGT GGA CCC CAG      308
84  Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser Cys Gly Pro Gln
85 35 40 45
90  TGT CAT AAG GGA ACT CCA CTG CCC ACT TAC AAA GAA GCC AAG CAA TAT      356
91  Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Lys Glu Ala Lys Gln Tyr
92 50 55 60 65
94  CTG TCT TAT GAA ACG CTC TAT GCC AAT GGC AGC CGC ACA GAG ACN CAG      404
W--> 95  Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr Glu Xaa Gln
96                                     70 75 80
98  GTG GGC ATC TAC ATC CTC AGC AGT AGT GGA GAT GGG GCC CAN CNC CGA      452
W--> 99  Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly Ala Xaa Xaa Arg
100                                     85 90 95
102  GAC TCA GGG TCT TCA GGA AAG TCT CGA AGG AAG CGG CAG ATT TAT GGC      500
103  Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly
104 100 105 110
106  TAT GAC AGC AGG TTC AGC ATT TTT GGG AAG GAC TTC CTG CTC AAC TAC      548
107  Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr
108 115 120 125
110  CCT TTC TCA ACA TCA GTG AAG TTA TCC ACG GGC TGC ACC GGC ACC CTG      596
111  Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu
112 130 135 140 145
114  GTG GCA GAA AAN CAT GTC CTC ACA GCT GCC CAC TGC ATA CAC GAT GGA      644
W--> 115  Val Ala Glu Xaa His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
116                                     150 155 160
118  AAA ACC TAT GTG AAA GGA ACC CAG AAG CTT CGA GTC GGC TTC CTA AAG      692
119  Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu Lys
120 165 170 175
122  CCC AAG TTT AAA GAT GGT GGT CGA GGG GCC AAC GAC TCC ACT TCA GCC      740
123  Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr Ser Ala
124 180 185 190
126  ATG CCC GAG CAG ATG AAA TTT CAG TGG ATC CGG GTG AAA CGC ACC CAT      788
127  Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys Arg Thr His
128 195 200 205
130  GTG CCC AAG GGT TGG ATC AAG GGC AAT GCC AAT GAC ATC GGC ATG GAT      836
131  Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp Ile Gly Met Asp
132 210 215 220 225

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136 TAT GAT TAT GCC CTC CTG GAA CTC AAA AAG CCC CAC AAG AGA AAA TTT      884
137 Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His Lys Arg Lys Phe
138                230                235                240
140 ATG AAG ATT GGG GTG AGC CCT CCT GCT AAG CAG CTG CCA GGG GGC AGA      932
141 Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro Gly Gly Arg
142                245                250                255
144 ATT CAC TTC TCT GGT TAT GAC AAT GAC CGA CCA GGC AAT TTG GTG TAT      980
145 Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn Leu Val Tyr
146                260                265                270
148 CGC TTC TGT GAC GTC AAA GAC GAG ACC TAT GAC TTG TTG TAC CAG CAA    1028
149 Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu Tyr Gln Gln
150                275                280                285
152 TGC GAT GCC CAG CCA GGG GCC AGC GGG TAT GGG GTA TAT GTG AGG ATG    1076
153 Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val Tyr Val Arg Met
154 290                295                300                305
156 TGG AAG AGA CAG CAG CAG AAG TGG GAG CGA AAA ATT ATT GGC ATT TTT    1124
157 Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe
158                310                315                320
160 TCA GGG CAC CAG TGG GTG GAC ATG AAT GGT TCC CCA CAG GAT TTC AAC    1172
161 Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn
162                325                330                335
164 GTG GCT GTC AGA ATC ACT CCT CTC AAA TAT GCC CAG ATC TGC TAT TGG    1220
165 Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp
166                340                345                350
168 ATT AAA GGA AAC TAC CTG GAT TGT AGG GAG GGT GAC ACA GTG TTC CTT    1268
169 Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp Thr Val Phe Leu
170                355                360                365
172 CCT GGC AGC AAT TAAGGTCTTC ATGTTCTTAT TTTAGGAGAG GCCAAATTGT TTTT    1325
173 Pro Gly Ser Asn
174 370
176 GTCATTGGCG TGCACACGTG TGTGTGTGTG TGTGTGTGTG TGTAAGGTGT CTTATAATCT    1385
177 TTTACCTATT TCTTACAATT GCAAGATGAC TGGCTTTACT ATTTGAAAAC TGGTTTGTGT    1445
178 ATCATATCAT ATATCATTTA AGCAGTTTGA AGGCATACTT TTGCATAGAA ATAAAAAAAA    1505
179 TACTGATTTG GGGCAATGAG GAATATTTGA CAATTAAGTT AATCTTCACG TTTTTCGAAA    1565
180 CTTTGATTTT TATTTTCATCT GAACTTGTTT CAAAGATTTA TATTAAATAT TTGGCATACA    1625
181 AGAGATATG                                1634
183 (2) INFORMATION FOR SEQ ID NO: 2:
185     (i) SEQUENCE CHARACTERISTICS:
186         (A) LENGTH: 392 amino acids
187         (B) TYPE: amino acid
188         (C) STRANDEDNESS: single
189         (D) TOPOLOGY: linear
191     (ii) MOLECULE TYPE: protein
192     (v) FRAGMENT TYPE: internal
193     (ix) FEATURE:
195         (A) NAME/KEY: Signal Sequence
196         (B) LOCATION: 1...19
197         (D) OTHER INFORMATION:
199     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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201 Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys
202                               -15                               -10                               -5
203 Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp
204                               1                               5                               10
205 Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu
206                               15                               20                               25
207 Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser
208                               30                               35                               40                               45
209 Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Lys Glu
210                               50                               55                               60
211 Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg
212                               65                               70                               75
W--> 213 Thr Glu Xaa Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly
214                               80                               85                               90
W--> 215 Ala Xaa Xaa Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg
216                               95                               100                               105
217 Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe
218                               110                               115                               120                               125
219 Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys
220                               130                               135                               140
W--> 221 Thr Gly Thr Leu Val Ala Glu Xaa His Val Leu Thr Ala Ala His Cys
222                               145                               150                               155
223 Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
224                               160                               165                               170
227 Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
228                               175                               180                               185
229 Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
230                               190                               195                               200                               205
231 Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
232                               210                               215                               220
233 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
234                               225                               230                               235
235 Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
236                               240                               245                               250
237 Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
238                               255                               260                               265
239 Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
240                               270                               275                               280                               285
241 Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val
242                               290                               295                               300
243 Tyr Val Arg Met Trp Lys Arg Gln Gln Lys Trp Glu Arg Lys Ile
244                               305                               310                               315
245 Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
246                               320                               325                               330
247 Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
248                               335                               340                               345
249 Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp
250                               350                               355                               360                               365
251 Thr Val Phe Leu Pro Gly Ser Asn

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252                               370
254 (2) INFORMATION FOR SEQ ID NO: 3:
256     (i) SEQUENCE CHARACTERISTICS:
257         (A) LENGTH: 17 base pairs
258         (B) TYPE: nucleic acid
259         (C) STRANDEDNESS: single
260         (D) TOPOLOGY: linear
263     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
265     TGYACNGGNW SNHTNRT                                     17
267 (2) INFORMATION FOR SEQ ID NO: 4:
269     (i) SEQUENCE CHARACTERISTICS:
270         (A) LENGTH: 17 base pairs
271         (B) TYPE: nucleic acid
272         (C) STRANDEDNESS: single
273         (D) TOPOLOGY: linear
276     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
278     AYNADNSWNC CNGTRCA                                     17
280 (2) INFORMATION FOR SEQ ID NO: 5:
282     (i) SEQUENCE CHARACTERISTICS:
283         (A) LENGTH: 17 base pairs
284         (B) TYPE: nucleic acid
285         (C) STRANDEDNESS: single
286         (D) TOPOLOGY: linear
289     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
291     ACNGCNGSNC AYTGYAT                                     17
293 (2) INFORMATION FOR SEQ ID NO: 6:
295     (i) SEQUENCE CHARACTERISTICS:
296         (A) LENGTH: 17 base pairs
297         (B) TYPE: nucleic acid
298         (C) STRANDEDNESS: single
299         (D) TOPOLOGY: linear
302     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
304     ATRCARTGNS CNGCNGT                                     17
306 (2) INFORMATION FOR SEQ ID NO: 7:
308     (i) SEQUENCE CHARACTERISTICS:
309         (A) LENGTH: 17 base pairs
310         (B) TYPE: nucleic acid
311         (C) STRANDEDNESS: single
312         (D) TOPOLOGY: linear
315     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
317     WYRTNCCNWV NGGNTGG                                     17
319 (2) INFORMATION FOR SEQ ID NO: 8:
321     (i) SEQUENCE CHARACTERISTICS:
322         (A) LENGTH: 17 base pairs
323         (B) TYPE: nucleic acid
324         (C) STRANDEDNESS: single
325         (D) TOPOLOGY: linear
328     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
330     CCANCCNBWN GGNAYRW                                     17

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